Example 4

Mapping of Nucleic Acid Sequences on the Human Genome

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server (http://www.stanford.edu/RH/rhserver_form2.html). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (http://gdbwww.dkfz-heidelberg.de).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the Gap between Genome Mapping and Genome Sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence Mapping by Electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (http://www.ebi.ac.uk/RHdb/index.html). Analogously to the mapping by the hybrid panels,

the results were evaluated with the above-mentioned software and
the software of the Whitehead Institute
(http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl).

TABLE I

Col. 1 - Sequence ID No.:

Col. 2 - Expression in hysteromyomic tissue:

Col. 3 - Function

Col. 4 - Modules

Col. 5 - Length of the applied sequence in bases

Col. 6 - Cytogenetic localization

Col. 7 - Next marker

[Key to Table I:]

[Col. 2:] erhöht = elevated

[Col. 3:]
    [Seq. ID No.: 14, 15, 17, 30, 31] unbekannt = unknown

    [Seq. ID No.: 16] Homolog zu Homo sapiens... = homologous
                     to homo sapiens...

    [Seq. ID No.: 18] Humanes Homolog zu ... = human homolog to

    [Seq. ID No.: 52] Verlängerung von Seq. ID. 14 =
                      Lengthening of Seq. ID. 14

TABLE I

TABELLE I

Sequenz ID No.	Expression im Uterus-Myomgewebe	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cytogenetische Lokalisation	nächster Marker
1	erhöht	Human mRNA for ornithine decarboxylase antizyme	"abhydrolase"	779		
2	erhöht	Human MEST mRNA		2310		D5S1730
3	erhöht	Human cocaine and amphetamine regulated transcript CART (hCART)		854	5q11.2-q13.1	
4	erhöht	Human microfibril-associated glycoprotein (MFAP2)		1112	1p36.11-p36.13	D2S387
5	erhöht	Human mRNA for KIAA0108 gene	"kazal"	1051	2p23.3	
6	erhöht	Human SPARC/osteonectin	"rrn"	1516	5q32-q33.1	Wi-9798
7	erhöht	Homo sapiens splicing factor, arginine/serine-rich 7 (SFRS7)		2367	2p22.3-p22.1	
8	erhöht	Human triosephosphate isomerase	3x "TIM"	568		
9	erhöht	Human nuclear ribonucleoprotein particle (hnRNP) C		1775		
10	erhöht	Human thymosin beta-4	"Thymosin"	509		
11	erhöht	Human growth hormone-dependent insulin-like growth factor-binding protein mRNA	"IGFBP", "thyroglobulin 1"	2191	7p12.2-p13	
12	erhöht	Human H19	"lipocalin"	1769		
13	erhöht	Human cellular retinoic acid-binding protein II (CRABP)	"rrn"	1026	14p11.2-14p11.1	WI-4204
14	erhöht	unbekannt		676		
15	erhöht	unbekannt		1254		
16	erhöht	Homolog zu Homo sapiens mRNA for putatively prenylated protein / unbekannt		537		
17	erhöht	Humanes Homolog zu P. vivax pval gene	5x "LRR"	823		
18	erhöht	Human tunican mRNA	"S2"	1082		
19	erhöht	Human 37 kD laminin receptor precursor/p40 ribosome associated protein		1540	12q21.31-12q21.33	D12S351
20	erhöht	Human YMP	"PMP22"	844		
21	erhöht	Human NADH:ubiquinone oxidoreductase MLRQ subunit		862	20q13.32-q13.33	
22	erhöht	Human mRNA for coupling protein G(s) alpha-subunit	"G-alpha", "arf"	546		
23	erhöht	Human hnRNP core protein A1	"rrm"	1591		
24	erhöht	Human HMG-17 gene for non-histone chromosomal protein	"HMG14_17"	441		
25	erhöht	H.sapiens mRNA for prolactin (clone PRL205)	"hormone"	1131		
26	erhöht			1071		
27	erhöht	Human mRNA for neurite outgrowth-promoting protein.	3x "PTN MK"	896		
28	erhöht	H.sapiens mRNA for proliferation-associated gene (pag)	"AhpC-TSA"	1050	1p32.3-p34.3	
29	erhöht	H.sapiens alpha NAC		581		
30	erhöht	unbekannt		264		
31	erhöht	unbekannt		111		
52	erhöht	Verlängerung von Seq. ID 14	"rrn"	3665	14p11.2-14p11.1	WI-4204

References to the modules:

Pfam: Protein families database of alignments and HMMs

~~(pfam@sanger.ac.uk)~~

PROSITE: The PROSITE database, its status in 1999. Nucleic

Acids Res. 27: 215-219 ~~(http://www.expasy.ch/sprot/prosite.html)~~

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